

# SEQUENCE LISTING

<110> Bayer Aktiengesellschaft

<120> Acetylcholine receptor subunits

<130> Le A 34 821

<140>

<141>

<150> DE 100 42 177.6

<151> 2000-08-28

<160> 17

<170> PatentIn Ver. 2.1

<210> 1

<211> 45

<212> PRT

<213> Torpedo californica

<400> 1

Asp	Phe	Ala	Ile	Val	His	Met	Thr	Lys	Leu	Leu	Leu	Asp	Tyr	Thr	Gly
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Lys	Ile	Met	Trp	Thr	Pro	Pro	Ala	Ile	Phe	Lys	Ser	Tyr	Cys	Glu	Ile
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Ile	Val	Thr	His	Phe	Pro	Phe	Asp	Gln	Gln	Asn	Cys	Thr
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<210> 2

<211> 1869

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1866)

<220>

<223> Description of Artificial Sequence: Modified alpha  
4 subunit of the chicken nicotinic acetylcholine  
receptor

<400> 2

atg	gga	ttt	ctc	gtg	tcg	aag	gga	aac	ctc	ctc	ctc	ctg	ctg	tgt	gcc	48
Met	Gly	Phe	Leu	Val	Ser	Lys	Gly	Asn	Leu	Leu	Leu	Leu	Leu	Cys	Ala	
1				5					10					15		

agc atc ttc ccc gct ttc ggc cac gtg gaa acg cga gcc cat gcg gag	96
Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu	
20 25 30	
gag cgc ctc ctg aag aaa ctc ttc tcc ggg tat aac aag tgg tcc cgt	144
Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg	
35 40 45	
ccc gtc gcc aac att tcg gat gtg gtc ctg gtc cgc ttc ggc ttg tcc	192
Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser	
50 55 60	
ata gcc cag ctc atc gat gtt gat gag aag aac caa atg atg acc aca	240
Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr	
65 70 75 80	
aat gtg tgg gtg aag cag gag tgg cac gac tac aag ctg cgc tgg gac	288
Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp	
85 90 95	
ccc cag gag tat gaa aac gtc aca tcc atc cga atc ccc tca gag ctc	336
Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu	
100 105 110	
atc tgg cgg ccg gac ata gtc ctc tac aac aat gcc gac ggc aac ttc	384
Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asn Phe	
115 120 125	
gag gta acg ctg gcg acg aag gcg act ttg aat tat acg gga cgt gtg	432
Glu Val Thr Leu Ala Thr Lys Ala Thr Leu Asn Tyr Thr Gly Arg Val	
130 135 140	
gag tgg cgc ccg ccg gct atc tac aag tcc tcg tgc gag atc gac gtg	480
Glu Trp Arg Pro Pro Ala Ile Tyr Lys Ser Ser Cys Glu Ile Asp Val	
145 150 155 160	
gaa tac ttc ccg ttc gac cag cag acg tgc gtc atg aag ttc ggc tcg	528
Glu Tyr Phe Pro Phe Asp Gln Gln Thr Cys Val Met Lys Phe Gly Ser	
165 170 175	
tgg aca tat gac aaa gct aag ata gac ttg gtg agc atg cat agc cat	576
Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His	
180 185 190	
gtg gac caa ctg gac tac tgg gaa agc ggg gag tgg gtc atc att aat	624
Val Asp Gln Leu Asp Tyr Trp Glu Ser Gly Glu Trp Val Ile Ile Asn	
195 200 205	
gcc gtg ggc aat tac aac agc aag aaa tat gaa tgc tgc aca gag atc	672
Ala Val Gly Asn Tyr Asn Ser Lys Lys Tyr Glu Cys Cys Thr Glu Ile	
210 215 220	
tac cct gat ata act tac tcc ttc att atc cgg agg ctg ccg ctg ttc	720
Tyr Pro Asp Ile Thr Tyr Ser Phe Ile Ile Arg Arg Leu Pro Leu Phe	

225	230							235							240			
tac aca atc aat ttg atc att ccc tgc ctg ctt atc tcc tgc ttg act	Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr							245 250 255										768
gtc ctg gtc ttc tac cta ccc tct gag tgc gga gag aag ata acc ttg	Val Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Ile Thr Leu							260 265 270										816
tgc atc tct gtg ctg cta tcc ctc acg gtg ttc ctg ctg ctc atc aca	Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Leu Ile Thr							275 280 285										864
gag atc atc cct tct acc tcc ctg gtc atc ccc ctg ata gga gag tat	Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro Leu Ile Gly Glu Tyr							290 295 300										912
ctg ctc ttc acc atg ata ttt gtc acc ttg tct atc atc atc act gtc	Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Ile Ile Thr Val							305 310 315 320										960
ttt gtg ctc aac gta cac cac cgt tca cca cgt acc cac acg atg cct	Phe Val Leu Asn Val His His Arg Ser Pro Arg Thr His Thr Met Pro							325 330 335										1008
gac tgg gtg agg agg gtc ttc ctt gac ata gtc cca cgt ctc ctc ttc	Asp Trp Val Arg Arg Val Phe Leu Asp Ile Val Pro Arg Leu Leu Phe							340 345 350										1056
atg aag cgg ccc tcc aca gtg aaa gac aat tgc aag aag ctt att gaa	Met Lys Arg Pro Ser Thr Val Lys Asp Asn Cys Lys Lys Leu Ile Glu							355 360 365										1104
tct atg cac aaa cta acc aac tca cca agg ctt tgg tct gag acc gac	Ser Met His Lys Leu Thr Asn Ser Pro Arg Leu Trp Ser Glu Thr Asp							370 375 380										1152
atg gag ccc aac ttc act acc tca tcc tcc ccc agc ccc cag agt aat	Met Glu Pro Asn Phe Thr Thr Ser Ser Ser Pro Ser Pro Gln Ser Asn							385 390 395 400										1200
gaa cct tca ccc aca tct tcc ttc tgt gcc cac ctt gag gag cca gcc	Glu Pro Ser Pro Thr Ser Ser Phe Cys Ala His Leu Glu Glu Pro Ala							405 410 415										1248
aaa cct atg tgc aaa tcc cct tct gga cag tac tca atg ctg cac cct	Lys Pro Met Cys Lys Ser Pro Ser Gly Gln Tyr Ser Met Leu His Pro							420 425 430										1296
gag ccc cca cag gtg acg tgt tcc tct ccg aag ccc tcc tgc cac ccc	Glu Pro Pro Gln Val Thr Cys Ser Ser Pro Lys Pro Ser Cys His Pro							435 440 445										1344

ctg	agt	gac	acc	cag	acc	aca	tct	atc	tca	aaa	ggc	aga	tcg	ctc	agt	1392
Leu	Ser	Asp	Thr	Gln	Thr	Thr	Ser	Ile	Ser	Lys	Gly	Arg	Ser	Leu	Ser	
450						455					460					
gtt	cag	cag	atg	tac	agc	ccc	aat	aag	aca	gag	gaa	ggg	agc	atc	cgc	1440
Val	Gln	Gln	Met	Tyr	Ser	Pro	Asn	Lys	Thr	Glu	Glu	Gly	Ser	Ile	Arg	
465					470					475					480	
tgt	agg	tcc	cga	agc	atc	cag	tac	tgt	tac	ctg	cag	gag	gac	tct	tcc	1488
Cys	Arg	Ser	Arg	Ser	Ile	Gln	Tyr	Cys	Tyr	Leu	Gln	Glu	Asp	Ser	Ser	
				485					490					495		
cag	acc	aat	ggc	cac	tct	agt	gcc	tct	cca	gcg	tcg	cag	cgc	tgc	cac	1536
Gln	Thr	Asn	Gly	His	Ser	Ser	Ala	Ser	Pro	Ala	Ser	Gln	Arg	Cys	His	
			500					505					510			
ctc	aat	gaa	gag	cag	ccc	cag	cac	aag	ccc	cac	cag	tgc	aag	tgt	aag	1584
Leu	Asn	Glu	Glu	Gln	Pro	Gln	His	Lys	Pro	His	Gln	Cys	Lys	Cys	Lys	
		515					520					525				
tgc	aga	aag	gga	gag	gca	gct	ggc	aca	ccg	act	caa	gga	agc	aag	agc	1632
Cys	Arg	Lys	Gly	Glu	Ala	Ala	Gly	Thr	Pro	Thr	Gln	Gly	Ser	Lys	Ser	
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cac	agc	aac	aaa	gga	gaa	cac	ctc	gtg	ctg	atg	tcc	cca	gcc	ctg	aag	1680
His	Ser	Asn	Lys	Gly	Glu	His	Leu	Val	Leu	Met	Ser	Pro	Ala	Leu	Lys	
545					550					555					560	
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Leu	Ala	Val	Glu	Gly	Val	His	Tyr	Ile	Ala	Asp	His	Leu	Arg	Ala	Glu	
				565					570					575		
gat	gca	gat	ttc	tca	gtg	aag	gaa	gac	tgg	aag	tac	gta	gca	atg	gtc	1776
Asp	Ala	Asp	Phe	Ser	Val	Lys	Glu	Asp	Trp	Lys	Tyr	Val	Ala	Met	Val	
			580					585					590			
att	gac	cgg	atc	ttt	ctc	tgg	atg	ttc	atc	atc	gtg	tgt	ttg	ctg	ggg	1824
Ile	Asp	Arg	Ile	Phe	Leu	Trp	Met	Phe	Ile	Ile	Val	Cys	Leu	Leu	Gly	
		595					600					605				
acc	gtt	ggg	ctc	ttc	ctc	ccg	ccg	tgg	ctg	gca	gga	atg	atc	taa		1869
Thr	Val	Gly	Leu	Phe	Leu	Pro	Pro	Trp	Leu	Ala	Gly	Met	Ile			
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<210> 3

<211> 622

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Modified alpha  
4 subunit of the chicken nicotinic acetylcholine  
receptor

<400> 3

Met	Gly	Phe	Leu	Val	Ser	Lys	Gly	Asn	Leu	Leu	Leu	Leu	Leu	Cys	Ala	
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Glu	Arg	Leu	Leu	Lys	Lys	Leu	Phe	Ser	Gly	Tyr	Asn	Lys	Trp	Ser	Arg	
		35					40					45				
Pro	Val	Ala	Asn	Ile	Ser	Asp	Val	Val	Leu	Val	Arg	Phe	Gly	Leu	Ser	
	50					55					60					
Ile	Ala	Gln	Leu	Ile	Asp	Val	Asp	Glu	Lys	Asn	Gln	Met	Met	Thr	Thr	
65					70					75					80	
Asn	Val	Trp	Val	Lys	Gln	Glu	Trp	His	Asp	Tyr	Lys	Leu	Arg	Trp	Asp	
				85					90					95		
Pro	Gln	Glu	Tyr	Glu	Asn	Val	Thr	Ser	Ile	Arg	Ile	Pro	Ser	Glu	Leu	
			100					105					110			
Ile	Trp	Arg	Pro	Asp	Ile	Val	Leu	Tyr	Asn	Asn	Ala	Asp	Gly	Asn	Phe	
		115					120					125				
Glu	Val	Thr	Leu	Ala	Thr	Lys	Ala	Thr	Leu	Asn	Tyr	Thr	Gly	Arg	Val	
	130					135					140					
Glu	Trp	Arg	Pro	Pro	Ala	Ile	Tyr	Lys	Ser	Ser	Cys	Glu	Ile	Asp	Val	
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Glu	Tyr	Phe	Pro	Phe	Asp	Gln	Gln	Thr	Cys	Val	Met	Lys	Phe	Gly	Ser	
				165					170					175		
Trp	Thr	Tyr	Asp	Lys	Ala	Lys	Ile	Asp	Leu	Val	Ser	Met	His	Ser	His	
			180					185					190			
Val	Asp	Gln	Leu	Asp	Tyr	Trp	Glu	Ser	Gly	Glu	Trp	Val	Ile	Ile	Asn	
		195					200					205				
Ala	Val	Gly	Asn	Tyr	Asn	Ser	Lys	Lys	Tyr	Glu	Cys	Cys	Thr	Glu	Ile	
	210					215					220					
Tyr	Pro	Asp	Ile	Thr	Tyr	Ser	Phe	Ile	Ile	Arg	Arg	Leu	Pro	Leu	Phe	
225					230					235					240	
Tyr	Thr	Ile	Asn	Leu	Ile	Ile	Pro	Cys	Leu	Leu	Ile	Ser	Cys	Leu	Thr	
				245					250					255		
Val	Leu	Val	Phe	Tyr	Leu	Pro	Ser	Glu	Cys	Gly	Glu	Lys	Ile	Thr	Leu	
			260					265					270			
Cys	Ile	Ser	Val	Leu	Leu	Ser	Leu	Thr	Val	Phe	Leu	Leu	Leu	Ile	Thr	
		275					280					285				

Glu	Ile	Ile	Pro	Ser	Thr	Ser	Leu	Val	Ile	Pro	Leu	Ile	Gly	Glu	Tyr
290						295					300				
Leu	Leu	Phe	Thr	Met	Ile	Phe	Val	Thr	Leu	Ser	Ile	Ile	Ile	Thr	Val
305					310					315					320
Phe	Val	Leu	Asn	Val	His	His	Arg	Ser	Pro	Arg	Thr	His	Thr	Met	Pro
			325						330					335	
Asp	Trp	Val	Arg	Arg	Val	Phe	Leu	Asp	Ile	Val	Pro	Arg	Leu	Leu	Phe
			340					345					350		
Met	Lys	Arg	Pro	Ser	Thr	Val	Lys	Asp	Asn	Cys	Lys	Lys	Leu	Ile	Glu
		355					360					365			
Ser	Met	His	Lys	Leu	Thr	Asn	Ser	Pro	Arg	Leu	Trp	Ser	Glu	Thr	Asp
	370					375					380				
Met	Glu	Pro	Asn	Phe	Thr	Thr	Ser	Ser	Ser	Pro	Ser	Pro	Gln	Ser	Asn
385					390					395					400
Glu	Pro	Ser	Pro	Thr	Ser	Ser	Phe	Cys	Ala	His	Leu	Glu	Glu	Pro	Ala
				405					410					415	
Lys	Pro	Met	Cys	Lys	Ser	Pro	Ser	Gly	Gln	Tyr	Ser	Met	Leu	His	Pro
			420					425					430		
Glu	Pro	Pro	Gln	Val	Thr	Cys	Ser	Ser	Pro	Lys	Pro	Ser	Cys	His	Pro
		435					440					445			
Leu	Ser	Asp	Thr	Gln	Thr	Thr	Ser	Ile	Ser	Lys	Gly	Arg	Ser	Leu	Ser
	450					455					460				
Val	Gln	Gln	Met	Tyr	Ser	Pro	Asn	Lys	Thr	Glu	Glu	Gly	Ser	Ile	Arg
465					470					475					480
Cys	Arg	Ser	Arg	Ser	Ile	Gln	Tyr	Cys	Tyr	Leu	Gln	Glu	Asp	Ser	Ser
				485					490					495	
Gln	Thr	Asn	Gly	His	Ser	Ser	Ala	Ser	Pro	Ala	Ser	Gln	Arg	Cys	His
			500					505					510		
Leu	Asn	Glu	Glu	Gln	Pro	Gln	His	Lys	Pro	His	Gln	Cys	Lys	Cys	Lys
		515					520					525			
Cys	Arg	Lys	Gly	Glu	Ala	Ala	Gly	Thr	Pro	Thr	Gln	Gly	Ser	Lys	Ser
	530					535					540				
His	Ser	Asn	Lys	Gly	Glu	His	Leu	Val	Leu	Met	Ser	Pro	Ala	Leu	Lys
545					550					555					560
Leu	Ala	Val	Glu	Gly	Val	His	Tyr	Ile	Ala	Asp	His	Leu	Arg	Ala	Glu
				565					570					575	

Asp	Ala	Asp	Phe	Ser	Val	Lys	Glu	Asp	Trp	Lys	Tyr	Val	Ala	Met	Val
			580					585					590		
Ile	Asp	Arg	Ile	Phe	Leu	Trp	Met	Phe	Ile	Ile	Val	Cys	Leu	Leu	Gly
		595					600					605			
Thr	Val	Gly	Leu	Phe	Leu	Pro	Pro	Trp	Leu	Ala	Gly	Met	Ile		
	610					615					620				

<210> 4  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 4  
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<210> 5  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 5  
 gtcatatgtc cacgagccga ac 22

<210> 6  
 <211> 1896  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)..(1893)

<220>  
 <223> Description of Artificial Sequence: Modified alpha  
 4 subunit of the chicken nicotinic acetylcholine  
 receptor

<400> 6  
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 Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Leu Cys Ala  
 1 5 10 15





225				230				235				240				
ttc	att	atc	cgg	agg	ctg	cgg	ctg	ttc	tac	aca	atc	aat	ttg	atc	att	768
Phe	Ile	Ile	Arg	Arg	Leu	Pro	Leu	Phe	Tyr	Thr	Ile	Asn	Leu	Ile	Ile	
				245					250					255		
ccc	tgc	ctg	ctt	atc	tcc	tgc	ttg	act	gtc	ctg	gtc	ttc	tac	cta	ccc	816
Pro	Cys	Leu	Leu	Ile	Ser	Cys	Leu	Thr	Val	Leu	Val	Phe	Tyr	Leu	Pro	
				260					265					270		
tct	gag	tgc	gga	gag	aag	ata	acc	ttg	tgc	atc	tct	gtg	ctg	cta	tcc	864
Ser	Glu	Cys	Gly	Glu	Lys	Ile	Thr	Leu	Cys	Ile	Ser	Val	Leu	Leu	Ser	
				275					280					285		
ctc	acg	gtg	ttc	ctg	ctg	ctc	atc	aca	gag	atc	atc	cct	tct	acc	tcc	912
Leu	Thr	Val	Phe	Leu	Leu	Leu	Ile	Thr	Glu	Ile	Ile	Pro	Ser	Thr	Ser	
				290					295					300		
ctg	gtc	atc	ccc	ctg	ata	gga	gag	tat	ctg	ctc	ttc	acc	atg	ata	ttt	960
Leu	Val	Ile	Pro	Leu	Ile	Gly	Glu	Tyr	Leu	Leu	Phe	Thr	Met	Ile	Phe	
				305					310					315		
gtc	acc	ttg	tct	atc	atc	atc	act	gtc	ttt	gtg	ctc	aac	gta	cac	cac	1008
Val	Thr	Leu	Ser	Ile	Ile	Ile	Thr	Val	Phe	Val	Leu	Asn	Val	His	His	
				325					330					335		
cgt	tca	cca	cgt	acc	cac	acg	atg	cct	gac	tgg	gtg	agg	agg	gtc	ttc	1056
Arg	Ser	Pro	Arg	Thr	His	Thr	Met	Pro	Asp	Trp	Val	Arg	Arg	Val	Phe	
				340					345					350		
ctt	gac	ata	gtc	cca	cgt	ctc	ctc	ttc	atg	aag	cgg	ccc	tcc	aca	gtg	1104
Leu	Asp	Ile	Val	Pro	Arg	Leu	Leu	Phe	Met	Lys	Arg	Pro	Ser	Thr	Val	
				355					360					365		
aaa	gac	aat	tgc	aag	aag	ctt	att	gaa	tct	atg	cac	aaa	cta	acc	aac	1152
Lys	Asp	Asn	Cys	Lys	Lys	Leu	Ile	Glu	Ser	Met	His	Lys	Leu	Thr	Asn	
				370					375					380		
tca	cca	agg	ctt	tgg	tct	gag	acc	gac	atg	gag	ccc	aac	ttc	act	acc	1200
Ser	Pro	Arg	Leu	Trp	Ser	Glu	Thr	Asp	Met	Glu	Pro	Asn	Phe	Thr	Thr	
				385					390					395		
tca	tcc	tcc	ccc	agc	ccc	cag	agt	aat	gaa	cct	tca	ccc	aca	tct	tcc	1248
Ser	Ser	Ser	Pro	Ser	Pro	Gln	Ser	Asn	Glu	Pro	Ser	Pro	Thr	Ser	Ser	
				405					410					415		
ttc	tgt	gcc	cac	ctt	gag	gag	cca	gcc	aaa	cct	atg	tgc	aaa	tcc	cct	1296
Phe	Cys	Ala	His	Leu	Glu	Glu	Pro	Ala	Lys	Pro	Met	Cys	Lys	Ser	Pro	
				420					425					430		
tct	gga	cag	tac	tca	atg	ctg	cac	cct	gag	ccc	cca	cag	gtg	acg	tgt	1344
Ser	Gly	Gln	Tyr	Ser	Met	Leu	His	Pro	Glu	Pro	Pro	Gln	Val	Thr	Cys	
				435					440					445		

tcc Ser	tct Ser 450	ccg Pro	aag Lys	ccc Pro	tcc Ser	tgc Cys 455	cac His	ccc Pro	ctg Leu	agt Ser	gac Asp 460	acc Thr	cag Gln	acc Thr	aca Thr	1392
tct Ser 465	atc Ile	tca Ser	aaa Lys	ggc Gly	aga Arg 470	tcg Ser	ctc Leu	agt Ser	gtt Val	cag Gln 475	cag Gln	atg Met	tac Tyr	agc Ser	ccc Pro 480	1440
aat Asn	aag Lys	aca Thr	gag Glu	gaa Glu 485	ggg Gly	agc Ser	atc Ile	cgc Arg	tgt Cys 490	agg Arg	tcc Ser	cga Arg	agc Ser	atc Ile 495	cag Gln	1488
tac Tyr	tgt Cys	tac Tyr	ctg Leu 500	cag Gln	gag Glu	gac Asp	tct Ser	tcc Ser 505	cag Gln	acc Thr	aat Asn	ggc Gly 510	cac His	tct Ser	agt Ser	1536
gcc Ala	tct Ser	cca Pro 515	gcg Ala	tcg Ser	cag Gln	cgc Arg	tgc Cys 520	cac His	ctc Leu	aat Asn	gaa Glu 525	gag Glu	cag Gln	ccc Pro	cag Gln	1584
cac His	aag Lys 530	ccc Pro	cac His	cag Gln	tgc Cys	aag Lys 535	tgt Cys	aag Lys	tgc Cys	aga Arg	aag Lys 540	gga Gly	gag Glu	gca Ala	gct Ala	1632
ggc Gly 545	aca Thr	ccg Pro	act Thr	caa Gln	gga Gly 550	agc Ser	aag Lys	agc Ser	cac His	agc Ser 555	aac Asn	aaa Lys	gga Gly	gaa Glu	cac His 560	1680
ctc Leu	gtg Val	ctg Leu	atg Met	tcc Ser 565	cca Pro	gcc Ala	ctg Leu	aag Lys	ctg Leu 570	gcg Ala	gtg Val	gaa Glu	ggg Gly	gtc Val 575	cac His	1728
tac Tyr	att Ile	gca Ala	gac Asp 580	cac His	ctg Leu	cga Arg	gca Ala	gaa Glu 585	gat Asp	gca Ala	gat Asp	ttc Phe	tca Ser 590	gtg Val	aag Lys	1776
gaa Glu	gac Asp	tgg Trp 595	aag Lys	tac Tyr	gta Val	gca Ala	atg Met 600	gtc Val	att Ile	gac Asp	cgg Arg 605	atc Ile	ttt Phe	ctc Leu	tgg Trp	1824
atg Met	ttc Phe 610	atc Ile	atc Ile	gtg Val	tgt Cys	ttg Leu 615	ctg Leu	ggg Gly	acc Thr	gtt Val	ggg Gly 620	ctc Leu	ttc Phe	ctc Leu	ccg Pro	1872
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<210> 7

<212> PRT

<223> Description of Arti

# 4 subunit of the chicken nicotinic acetylcholine receptor

<400> 7

Met	Gly	Phe	Leu	Val	Ser	Lys	Gly	Asn	Leu	Leu	Leu	Leu	Leu	Cys	Ala
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Ser	Ile	Phe	Pro	Ala	Phe	Gly	His	Val	Glu	Thr	Arg	Ala	His	Ala	Glu
			20					25					30		
Glu	Arg	Leu	Leu	Lys	Lys	Leu	Phe	Ser	Gly	Tyr	Asn	Lys	Trp	Ser	Arg
		35					40					45			
Pro	Val	Ala	Asn	Ile	Ser	Asp	Val	Val	Leu	Val	Arg	Phe	Gly	Leu	Ser
		50				55					60				
Ile	Ala	Gln	Leu	Ile	Asp	Val	Asp	Glu	Lys	Asn	Gln	Met	Met	Thr	Thr
	65				70					75					80
Asn	Val	Trp	Val	Lys	Gln	Glu	Trp	His	Asp	Tyr	Lys	Leu	Arg	Trp	Asp
				85					90					95	
Pro	Gln	Glu	Tyr	Glu	Asn	Val	Thr	Ser	Ile	Arg	Ile	Pro	Ser	Glu	Leu
			100					105					110		
Ile	Trp	Arg	Pro	Asp	Ile	Val	Leu	Tyr	Asn	Asn	Ala	Asp	Gly	Asp	Phe
		115					120					125			
Ala	Val	Thr	His	Leu	Thr	Lys	Ala	His	Leu	Phe	Tyr	Asp	Gly	Arg	Ile
		130				135					140				
Lys	Trp	Met	Pro	Pro	Ala	Ile	Tyr	Lys	Ser	Ser	Cys	Ser	Ile	Asp	Val
	145				150					155					160
Thr	Phe	Phe	Pro	Phe	Asp	Gln	Gln	Asn	Cys	Lys	Met	Lys	Phe	Gly	Ser
				165					170					175	
Trp	Thr	Tyr	Asp	Lys	Ala	Lys	Ile	Asp	Leu	Val	Ser	Met	His	Ser	His
			180					185					190		
Arg	Gly	Thr	Asn	Val	Val	Glu	Leu	Gly	Val	Asp	Gln	Leu	Asp	Tyr	Trp
		195					200					205			
Glu	Ser	Gly	Glu	Trp	Val	Ile	Ile	Asn	Ala	Val	Gly	Asn	Tyr	Asn	Ser
	210					215					220				
Lys	Lys	Tyr	Glu	Cys	Cys	Thr	Glu	Ile	Tyr	Pro	Asp	Ile	Thr	Tyr	Ser
	225				230					235					240
Phe	Ile	Ile	Arg	Arg	Leu	Pro	Leu	Phe	Tyr	Thr	Ile	Asn	Leu	Ile	Ile
				245					250					255	
Pro	Cys	Leu	Leu	Ile	Ser	Cys	Leu	Thr	Val	Leu	Val	Phe	Tyr	Leu	Pro
			260					265					270		

Ser	Glu	Cys	Gly	Glu	Lys	Ile	Thr	Leu	Cys	Ile	Ser	Val	Leu	Leu	Ser
		275					280					285			
Leu	Thr	Val	Phe	Leu	Leu	Leu	Ile	Thr	Glu	Ile	Ile	Pro	Ser	Thr	Ser
	290					295					300				
Leu	Val	Ile	Pro	Leu	Ile	Gly	Glu	Tyr	Leu	Leu	Phe	Thr	Met	Ile	Phe
305					310					315					320
Val	Thr	Leu	Ser	Ile	Ile	Ile	Thr	Val	Phe	Val	Leu	Asn	Val	His	His
				325					330					335	
Arg	Ser	Pro	Arg	Thr	His	Thr	Met	Pro	Asp	Trp	Val	Arg	Arg	Val	Phe
			340					345					350		
Leu	Asp	Ile	Val	Pro	Arg	Leu	Leu	Phe	Met	Lys	Arg	Pro	Ser	Thr	Val
		355					360					365			
Lys	Asp	Asn	Cys	Lys	Lys	Leu	Ile	Glu	Ser	Met	His	Lys	Leu	Thr	Asn
	370					375					380				
Ser	Pro	Arg	Leu	Trp	Ser	Glu	Thr	Asp	Met	Glu	Pro	Asn	Phe	Thr	Thr
385					390					395					400
Ser	Ser	Ser	Pro	Ser	Pro	Gln	Ser	Asn	Glu	Pro	Ser	Pro	Thr	Ser	Ser
				405					410					415	
Phe	Cys	Ala	His	Leu	Glu	Glu	Pro	Ala	Lys	Pro	Met	Cys	Lys	Ser	Pro
			420					425					430		
Ser	Gly	Gln	Tyr	Ser	Met	Leu	His	Pro	Glu	Pro	Pro	Gln	Val	Thr	Cys
		435					440					445			
Ser	Ser	Pro	Lys	Pro	Ser	Cys	His	Pro	Leu	Ser	Asp	Thr	Gln	Thr	Thr
		450				455					460				
Ser	Ile	Ser	Lys	Gly	Arg	Ser	Leu	Ser	Val	Gln	Gln	Met	Tyr	Ser	Pro
465					470					475					480
Asn	Lys	Thr	Glu	Glu	Gly	Ser	Ile	Arg	Cys	Arg	Ser	Arg	Ser	Ile	Gln
				485					490					495	
Tyr	Cys	Tyr	Leu	Gln	Glu	Asp	Ser	Ser	Gln	Thr	Asn	Gly	His	Ser	Ser
			500					505					510		
Ala	Ser	Pro	Ala	Ser	Gln	Arg	Cys	His	Leu	Asn	Glu	Glu	Gln	Pro	Gln
			515				520					525			
His	Lys	Pro	His	Gln	Cys	Lys	Cys	Lys	Cys	Arg	Lys	Gly	Glu	Ala	Ala
	530					535					540				
Gly	Thr	Pro	Thr	Gln	Gly	Ser	Lys	Ser	His	Ser	Asn	Lys	Gly	Glu	His
545					550					555					560



<223> Description of Artificial Sequence: Modified alpha  
4 subunit of the chicken nicotinic acetylcholine  
receptor

<400> 10

atg gga ttt ctc gtg tcg aag gga aac ctc ctc ctc ctg ctg tgt gcc	48
Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Leu Cys Ala	
1 5 10 15	
agc atc ttc ccc gct ttc ggc cac gtg gaa acg cga gcc cat gcg gag	96
Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu	
20 25 30	
gag cgc ctc ctg aag aaa ctc ttc tcc ggg tat aac aag tgg tcc cgt	144
Glu Arg Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg	
35 40 45	
ccc gtc gcc aac att tcg gat gtg gtc ctg gtc cgc ttc ggc ttg tcc	192
Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser	
50 55 60	
ata gcc cag ctc atc gat gtt gat gag aag aac caa atg atg acc aca	240
Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr	
65 70 75 80	
aat gtg tgg gtg aag cag gag tgg cac gac tac aag ctg cgc tgg gac	288
Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp	
85 90 95	
ccc cag gag tat gaa aac gtc aca tcc atc cga atc ccc tca gag ctc	336
Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu	
100 105 110	
atc tgg agg ccg gac att gtc cta tac aac aat gct gat ggt gac ttt	384
Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe	
115 120 125	
gca gtc acc cac ctg acc aaa gcc cac ctc ttc tat gat ggg aga att	432
Ala Val Thr His Leu Thr Lys Ala His Leu Phe Tyr Asp Gly Arg Ile	
130 135 140	
aaa tgg atg cca cct gcc atc tac aaa agc tcc tgc agc atc gat gtt	480
Lys Trp Met Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser Ile Asp Val	
145 150 155 160	
acc ttc ttc ccc ttt gat cag caa aac tgt aaa atg aaa ttt ggc tct	528
Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Lys Met Lys Phe Gly Ser	
165 170 175	
tgg aca tat gac aaa gct aag ata gac ttg gtg agc atg cat agc cat	576
Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His	
180 185 190	
gtc gac ctg tcc gag ttc tac acc tcc gtg gag tgg gac atc ctg gag	624

Val	Asp	Leu 195	Ser	Glu	Phe	Tyr	Thr 200	Ser	Val	Glu	Trp	Asp 205	Ile	Leu	Glu	
gtg	cca	gcc	gtc	agg	aac	gag	aag	ttc	tac	acg	tgc	tgc	gac	gag	ccc	672
Val	Pro 210	Ala	Val	Arg	Asn	Glu 215	Lys	Phe	Tyr	Thr	Cys 220	Cys	Asp	Glu	Pro	
tac	ctg	gac	ata	acg	ttt	aac	ttc	att	atc	cgg	agg	ctg	ccg	ctg	ttc	720
Tyr 225	Leu	Asp	Ile	Thr	Phe 230	Asn	Phe	Ile	Ile	Arg 235	Arg	Leu	Pro	Leu	Phe 240	
tac	aca	atc	aat	ttg	atc	att	ccc	tgc	ctg	ctt	atc	tcc	tgc	ttg	act	768
Tyr	Thr	Ile	Asn	Leu 245	Ile	Ile	Pro	Cys	Leu 250	Leu	Ile	Ser	Cys	Leu 255	Thr	
gtc	ctg	gtc	ttc	tac	cta	ccc	tct	gag	tgc	gga	gag	aag	ata	acc	ttg	816
Val	Leu	Val	Phe 260	Tyr	Leu	Pro	Ser	Glu 265	Cys	Gly	Glu	Lys	Ile 270	Thr	Leu	
tgc	atc	tct	gtg	ctg	cta	tcc	ctc	acg	gtg	ttc	ctg	ctg	ctc	atc	aca	864
Cys	Ile	Ser 275	Val	Leu	Leu	Ser	Leu 280	Thr	Val	Phe	Leu	Leu 285	Leu	Ile	Thr	
gag	atc	atc	cct	tct	acc	tcc	ctg	gtc	atc	ccc	ctg	ata	gga	gag	tat	912
Glu	Ile 290	Ile	Pro	Ser	Thr	Ser 295	Leu	Val	Ile	Pro	Leu 300	Ile	Gly	Glu	Tyr	
ctg	ctc	ttc	acc	atg	ata	ttt	gtc	acc	ttg	tct	atc	atc	atc	act	gtc	960
Leu 305	Leu	Phe	Thr	Met	Ile 310	Phe	Val	Thr	Leu	Ser 315	Ile	Ile	Ile	Thr	Val 320	
ttt	gtg	ctc	aac	gta	cac	cac	cgt	tca	cca	cgt	acc	cac	acg	atg	cct	1008
Phe	Val	Leu	Asn	Val 325	His	His	Arg	Ser	Pro 330	Arg	Thr	His	Thr	Met 335	Pro	
gac	tgg	gtg	agg	agg	gtc	ttc	ctt	gac	ata	gtc	cca	cgt	ctc	ctc	ttc	1056
Asp	Trp	Val	Arg 340	Arg	Val	Phe	Leu	Asp 345	Ile	Val	Pro	Arg	Leu 350	Leu	Phe	
atg	aag	cgg	ccc	tcc	aca	gtg	aaa	gac	aat	tgc	aag	aag	ctt	att	gaa	1104
Met	Lys	Arg 355	Pro	Ser	Thr	Val	Lys 360	Asp	Asn	Cys	Lys	Lys 365	Leu	Ile	Glu	
tct	atg	cac	aaa	cta	acc	aac	tca	cca	agg	ctt	tgg	tct	gag	acc	gac	1152
Ser	Met 370	His	Lys	Leu	Thr	Asn 375	Ser	Pro	Arg	Leu	Trp 380	Ser	Glu	Thr	Asp	
atg	gag	ccc	aac	ttc	act	acc	tca	tcc	tcc	ccc	agc	ccc	cag	agt	aat	1200
Met 385	Glu	Pro	Asn	Phe	Thr 390	Thr	Ser	Ser	Ser	Pro 395	Ser	Pro	Gln	Ser	Asn 400	
gaa	cct	tca	ccc	aca	tct	tcc	ttc	tgt	gcc	cac	ctt	gag	gag	cca	gcc	1248
Glu	Pro	Ser	Pro	Thr 405	Ser	Ser	Phe	Cys	Ala 410	His	Leu	Glu	Glu	Pro 415	Ala	

aaa Lys	cct Pro	atg Met	tgc Cys 420	aaa Lys	tcc Ser	cct Pro	tct Ser	gga Gly 425	cag Gln	tac Tyr	tca Ser	atg Met	ctg Leu 430	cac His	cct Pro	1296
gag Glu	ccc Pro	cca Pro 435	cag Gln	gtg Val	acg Thr	tgt Cys	tcc Ser 440	tct Ser	ccg Pro	aag Lys	ccc Pro	tcc Ser 445	tgc Cys	cac His	ccc Pro	1344
ctg Leu	agt Ser 450	gac Asp	acc Thr	cag Gln	acc Thr	aca Thr 455	tct Ser	atc Ile	tca Ser	aaa Lys	ggc Gly 460	aga Arg	tcg Ser	ctc Leu	agt Ser	1392
gtt Val 465	cag Gln	cag Gln	atg Met	tac Tyr	agc Ser 470	ccc Pro	aat Asn	aag Lys	aca Thr	gag Glu 475	gaa Glu	ggg Gly	agc Ser	atc Ile	cgc Arg 480	1440
tgt Cys	agg Arg	tcc Ser	cga Arg	agc Ser 485	atc Ile	cag Gln	tac Tyr	tgt Cys	tac Tyr 490	ctg Leu	cag Gln	gag Glu	gac Asp 495	tct Ser	tcc Ser	1488
cag Gln	acc Thr	aat Asn	ggc Gly 500	cac His	tct Ser	agt Ser	gcc Ala	tct Ser 505	cca Pro	gcg Ala	tcg Ser	cag Gln	cgc Arg 510	tgc Cys	cac His	1536
ctc Leu	aat Asn	gaa Glu 515	gag Glu	cag Gln	ccc Pro	cag Gln	cac His 520	aag Lys	ccc Pro	cac His	cag Gln	tgc Cys 525	aag Lys	tgt Cys	aag Lys	1584
tgc Cys	aga Arg 530	aag Lys	gga Gly	gag Glu	gca Ala 535	gct Ala	ggc Gly	aca Thr	ccg Pro	act Thr	caa Gln 540	gga Gly	agc Ser	aag Lys	agc Ser	1632
cac His 545	agc Ser	aac Asn	aaa Lys	gga Gly	gaa Glu 550	cac His	ctc Leu	gtg Val	ctg Leu	atg Met 555	tcc Ser	cca Pro	gcc Ala	ctg Leu	aag Lys 560	1680
ctg Leu	gcg Ala	gtg Val	gaa Glu	ggg Gly 565	gtc Val	cac His	tac Tyr	att Ile	gca Ala 570	gac Asp	cac His	ctg Leu	cga Arg	gca Ala 575	gaa Glu	1728
gat Asp	gca Ala	gat Asp	ttc Phe 580	tca Ser	gtg Val	aag Lys	gaa Glu	gac Asp 585	tgg Trp	aag Lys	tac Tyr	gta Val	gca Ala 590	atg Met	gtc Val	1776
att Ile	gac Asp	cgg Arg 595	atc Ile	ttt Phe	ctc Leu	tgg Trp	atg Met 600	ttc Phe	atc Ile	atc Ile	gtg Val	tgt Cys 605	ttg Leu	ctg Leu	ggg Gly	1824
acc Thr	gtt Val 610	ggg Gly	ctc Leu	ttc Phe	ctc Leu	ccg Pro 615	ccg Pro	tgg Trp	ctg Leu	gca Ala	gga Gly 620	atg Met	atc Ile	taa		1869



<210> 11  
 <211> 622  
 <212> PRT  
 <213> Artificial Sequence  
 <223> Description of Artificial Sequence: Modified alpha  
 4 subunit of the chicken nicotinic acetylcholine  
 receptor

<400> 11  
 Met Gly Phe Leu Val Ser Lys Gly Asn Leu Leu Leu Leu Leu Cys Ala  
 1 5 10 15  
 Ser Ile Phe Pro Ala Phe Gly His Val Glu Thr Arg Ala His Ala Glu  
 20 25 30  
 Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg  
 35 40 45  
 Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe Gly Leu Ser  
 50 55 60  
 Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr  
 65 70 75 80  
 Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp  
 85 90 95  
 Pro Gln Glu Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu  
 100 105 110  
 Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe  
 115 120 125  
 Ala Val Thr His Leu Thr Lys Ala His Leu Phe Tyr Asp Gly Arg Ile  
 130 135 140  
 Lys Trp Met Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser Ile Asp Val  
 145 150 155 160  
 Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Lys Met Lys Phe Gly Ser  
 165 170 175  
 Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met His Ser His  
 180 185 190  
 Val Asp Leu Ser Glu Phe Tyr Thr Ser Val Glu Trp Asp Ile Leu Glu  
 195 200 205  
 Val Pro Ala Val Arg Asn Glu Lys Phe Tyr Thr Cys Cys Asp Glu Pro  
 210 215 220  
 Tyr Leu Asp Ile Thr Phe Asn Phe Ile Ile Arg Arg Leu Pro Leu Phe  
 225 230 235 240

Tyr	Thr	Ile	Asn	Leu	Ile	Ile	Pro	Cys	Leu	Leu	Ile	Ser	Cys	Leu	Thr	245	250	255
Val	Leu	Val	Phe	Tyr	Leu	Pro	Ser	Glu	Cys	Gly	Glu	Lys	Ile	Thr	Leu	260	265	270
Cys	Ile	Ser	Val	Leu	Leu	Ser	Leu	Thr	Val	Phe	Leu	Leu	Leu	Ile	Thr	275	280	285
Glu	Ile	Ile	Pro	Ser	Thr	Ser	Leu	Val	Ile	Pro	Leu	Ile	Gly	Glu	Tyr	290	295	300
Leu	Leu	Phe	Thr	Met	Ile	Phe	Val	Thr	Leu	Ser	Ile	Ile	Ile	Thr	Val	305	310	315
Phe	Val	Leu	Asn	Val	His	His	Arg	Ser	Pro	Arg	Thr	His	Thr	Met	Pro	325	330	335
Asp	Trp	Val	Arg	Arg	Val	Phe	Leu	Asp	Ile	Val	Pro	Arg	Leu	Leu	Phe	340	345	350
Met	Lys	Arg	Pro	Ser	Thr	Val	Lys	Asp	Asn	Cys	Lys	Lys	Leu	Ile	Glu	355	360	365
Ser	Met	His	Lys	Leu	Thr	Asn	Ser	Pro	Arg	Leu	Trp	Ser	Glu	Thr	Asp	370	375	380
Met	Glu	Pro	Asn	Phe	Thr	Thr	Ser	Ser	Ser	Pro	Ser	Pro	Gln	Ser	Asn	385	390	395
Glu	Pro	Ser	Pro	Thr	Ser	Ser	Phe	Cys	Ala	His	Leu	Glu	Glu	Pro	Ala	405	410	415
Lys	Pro	Met	Cys	Lys	Ser	Pro	Ser	Gly	Gln	Tyr	Ser	Met	Leu	His	Pro	420	425	430
Glu	Pro	Pro	Gln	Val	Thr	Cys	Ser	Ser	Pro	Lys	Pro	Ser	Cys	His	Pro	435	440	445
Leu	Ser	Asp	Thr	Gln	Thr	Thr	Ser	Ile	Ser	Lys	Gly	Arg	Ser	Leu	Ser	450	455	460
Val	Gln	Gln	Met	Tyr	Ser	Pro	Asn	Lys	Thr	Glu	Glu	Gly	Ser	Ile	Arg	465	470	475
Cys	Arg	Ser	Arg	Ser	Ile	Gln	Tyr	Cys	Tyr	Leu	Gln	Glu	Asp	Ser	Ser	485	490	495
Gln	Thr	Asn	Gly	His	Ser	Ser	Ala	Ser	Pro	Ala	Ser	Gln	Arg	Cys	His	500	505	510
Leu	Asn	Glu	Glu	Gln	Pro	Gln	His	Lys	Pro	His	Gln	Cys	Lys	Cys	Lys	515	520	525

Cys Arg Lys Gly Glu Ala Ala Gly Thr Pro Thr Gln Gly Ser Lys Ser  
 530 535 540  
 His Ser Asn Lys Gly Glu His Leu Val Leu Met Ser Pro Ala Leu Lys  
 545 550 555 560  
 Leu Ala Val Glu Gly Val His Tyr Ile Ala Asp His Leu Arg Ala Glu  
 565 570 575  
 Asp Ala Asp Phe Ser Val Lys Glu Asp Trp Lys Tyr Val Ala Met Val  
 580 585 590  
 Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile Val Cys Leu Leu Gly  
 595 600 605  
 Thr Val Gly Leu Phe Leu Pro Pro Trp Leu Ala Gly Met Ile  
 610 615 620

<210> 12  
 <211> 79  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 12  
 caacagcaag aaatatgaat gctgcgacga gccctacctt gatataactt tcaacttcat 60  
 tatccggagg ctgccgctg 79

<210> 13  
 <211> 79  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 13  
 cagcggcagc ctccggataa tgaagttgaa agttatatca aggtagggct cgtcgcagca 60  
 ttcattttt ttgctgttg 79

<210> 14  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 14  
gaacaaaagc tggaggtcca ccgcggtggc 30

<210> 15  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 15  
gccaccgcg tggacctcca gcttttgttc 30

<210> 16  
<211> 75  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 16  
gcgggggagtg ggatcatctta gaagtcccgg ccgttcgcaa cgaaaagttt tatacatgct 60  
gcgacgagcc ctacc 75

<210> 17  
<211> 75  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 17  
ggtagggctc gtcgcagcat gtataaaact tttcgttgcg aacggccggg acttcaatga 60  
tgaccactc ccgc